

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

(ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
(F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/117,366
(B) FILING DATE: 07-SEP-1993
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: US 08/136,783
(B) FILING DATE: 14-OCT-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: P50186-2

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA 48
Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT 96
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30

GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT 144
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser

35	40	45	
GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA			192
Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro			
50	55	60	
GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT			240
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser			
65	70	75	80
GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC			288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr			
85	90	95	
CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT			336
Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys			
100	105	110	
CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG			384
Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu			
115	120	125	
GAA ATC AAA CGG			396
Glu Ile Lys Arg			
130			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Thr	Asp	Thr	Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1					5				10				15		

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
 20 25 30

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
 65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
 100 105 110

Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

Glu Ile Lys Arg
 130

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 64..483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA	60
GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA	108
Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala	
1 5 10 15	
TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG	156
Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu	
20 25 30	
CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA	204
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser	
35 40 45	
CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA	252
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly	
50 55 60	
AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC	300
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg	
65 70 75	
TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC	348
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser	
80 85 90 95	
AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT	396
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr	
100 105 110	
GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC	444
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe	
115 120 125	
GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA	483
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser	

130

135

140

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr
 1              5              10              15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
      20              25              30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
      35              40              45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
      50              55              60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
      65              70              75              80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
      85              90              95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
      100              105              110

Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
      115              120              125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
      130              135              140

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
GGT GCC TAC GGG	60
Gly Ala Tyr Gly	
20	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1 5 10 15
Gly Ala Tyr Gly
 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

GTC CAC TCC 57
Val His Ser

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG	96
Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu	
20 25 30	
CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA	144
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser	
35 40 45	
CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA	192
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly	
50 55 60	

AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC 240
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
65 70 75 80

TAT	AAC	CCA	TCC	CTG	AAG	AGC	CGG	CTC	ACA	ATC	TCC	AAG	GAT	ACC	TCC	288
Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	
				85				90					95			

AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT 336
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
100 105 110

GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC 384
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
115 120 125

GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA 423
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
20 25 30

Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
 35 40 45

 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
 50 55 60

 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
 65 70 75 80

 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
 85 90 95

 Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
 100 105 110

 Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
 115 120 125

 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT

48

Met	Val	Leu	Gln	Thr	Gln	Val	Phe	Ile	Ser	Leu	Leu	Leu	Trp	Ile	Ser	
1				5					10					15		
GGT	GCC	TAC	GGG	CAG	GTT	ACC	CTG	CGT	GAA	TCC	GGT	CCG	GCA	CTA	GTT	96
Gly	Ala	Tyr	Gly	Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	
			20					25					30			
AAA	CCG	ACC	CAG	ACC	CTG	ACG	TTA	ACC	TGC	ACC	TTC	TCC	GGT	TTC	TCC	144
Lys	Pro	Thr	Gln	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	
		35					40					45				
CTG	TCG	ACC	TCC	GGT	ATG	GGT	GTT	TCC	TGG	ATC	CGT	CAG	CCG	CCG	GGT	192
Leu	Ser	Thr	Ser	Gly	Met	Gly	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	
	50					55					60					
AAA	GGT	CTA	GAA	TGG	CTG	GCT	CAC	ATC	TAC	TGG	GAC	GAC	GAC	AAA	CGT	240
Lys	Gly	Leu	Glu	Trp	Leu	Ala	His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	
65					70					75					80	
TAC	AAC	CCG	AGC	CTG	AAA	TCC	CGT	CTG	ACG	ATA	TCC	AAA	GAC	ACC	TCC	288
Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	
			85						90					95		
CGT	AAC	CAG	GTT	GTT	CTG	ACC	ATG	ACT	AAC	ATG	GAC	CCG	GTT	GAC	ACC	336
Arg	Asn	Gln	Val	Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	
		100						105					110			
GCT	ACC	TAC	TAC	TGC	GCT	CGA	CGC	GAA	ACC	GTT	TTC	TAC	TGG	TAC	TTC	384
Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Arg	Glu	Thr	Val	Phe	Tyr	Trp	Tyr	Phe	
		115					120					125				
GAC	GTT	TGG	GGT	CGT	GGT	ACC	CCA	GTT	ACC	GTG	AGC	TCA				423
Asp	Val	Trp	Gly	Arg	Gly	Thr	Pro	Val	Thr	Val	Ser	Ser				
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1               5               10               15

Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val
      20               25               30

Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
      35               40               45

Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly
      50               55               60

Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
      65               70               75               80

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
      85               90               95

Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr
      100               105               110

Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
      115               120               125

Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
      130               135               140

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
GTC CAC TCC GAT ATC GTG ATG ACC CAG TCT CCA GAC TCG CTA GCT GTG	96
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val	
20 25 30	
TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC AAG GCC TCC CAA AGT GTT	144
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val	
35 40 45	
GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG	192
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG	240
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly	
65 70 75 80	
GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC	288
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85 90 95	
ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG	336
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln	

100	105	110	
CAA AGT AAT GAG GAT CCT CCG AGG TTC GGC GGA GGG ACC AAG GTG GAG			384
Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Gly Thr Lys Val Glu			
115	120	125	
ATC AAA CGT			393
Ile Lys Arg			
130			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val			
20	25	30	
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val			
35	40	45	
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly			
50	55	60	
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly			
65	70	75	80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 100 105 110

Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Arg
 130

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC 45
 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCT	GCA	TCC	AAT	CTA	GAA	TCT
Ala	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Ser Asn Leu Glu Ser

1

5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAG CAA AGT AAT GAG GAT CCT CCG ACG

27

Gln Gln Ser Asn Glu Asp Pro Pro Thr

1

5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gln Gln Ser Asn Glu Asp Pro Pro Thr
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACT TCT GGT ATG GGT GTG AGC
Thr Ser Gly Met Gly Val Ser
1 5

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Gly Met Gly Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAC ATT TAC TGG GAT GAT GAC AAG CGC TAT AAC CCA TCC CTG AAG AGC 48
His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA GAG ACT GTG TTC TAC TGG TAC TTC GAT GTC
Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
1 5 10

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAG CAA AGT AAT GAG GAT CCT CCG AGG

27

Gln Gln Ser Asn Glu Asp Pro Pro Arg

1

5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Gln Ser Asn Glu Asp Pro Pro Arg

1

5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

36

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTACATATGC AAGGCTTACA ACCACAATC

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTTACCCTG CGTGAATCCG GTCCGGCACT AGTTAAACCG ACCCAGACCC TGACGTTAAC 60
CTGCACCTTC TCCGGTTTCT CCCTGTCGAC CTCCGGTATG GGTGTTTCCT GGATCCG 117

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCAGCCGCCG GGTAAAGGTC TAGAATGGCT GGCTCACATC TACTGGGACG ACGACAAACG 60
TTACAACCCG AGCCTGAAAT CCCGTCTGAC GATATCCAAA GACACCTCCC GTAACCAGGT 120

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTTCTGACC ATGGACCCGG TTGACACCGC TACCTACTAC TGCCTCGTC GCGAAACCGT 60

TTTCTACTGG TACTTCGACG TTTGGGGTCG TGGTACCCCA GTTACCGTGA GCTCCCAACC 120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCCGGCGGC TGACGGATCC AGGAA 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGTCAGAA CAACCTGGTT ACGG 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGGTTAC CCTGCGTGAA TCCGG

25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCAACCCTCG AGTGCCATTG A

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTAGCTGTGT CTCTGGGCGA GAGGGCCACC ATCAACTGCA AGG

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTTGCA GTT GATGGTGGCC CTCTCGCCCA GAGACACAG

39

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCGAGAGGCC TCCCAAAGTG TTGATTATGA TGGTGATAGT TATATGAACT GGTATCAGCA

60

GAAACCC

67

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTTTCTGC TGATACCACT TCATATAACT ATCACCATCA TAATCAACAC TTTGGGAGGC 60

CTC 63

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATACTACTGT CAGCAAAGTA ATGAGGATCC TCCGAGGTTC GCGGAGGGA C 51

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGTCCCT CCGCCGAACC TCGGAGGATC CTCATTACTT TGCTGACAGT AGT

53

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGCAGCCTC CTAAGTTGCT CATTACGCT GCATCCAATC TAGAATCTGG GGTAC

55

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCAGATTCT AGATTGGATG CAGCGTAAAT GAGCAACTTA GGAGGCTGCC C

51

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATTCGAGGA CGCCAGCAAC ATGGTGTTC AGACCCAGGT CTCATTTCT CTGTTGCTCT 60
GGATCTCTGG TGCCTACGGG CAG 83

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTAACCTGCC CGTAGGCACC AGAGATCCAG AGCAACAGAG AAATGAAGAC CTGGGTCTGC 60
AACACCATGT TGCTGGCGTC CTCG 84

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGGTTACCC TGAAAGAGTC

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAGTAGTCC TTGACCAG

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACCGTCT CCTCAGCTAG CACCAAGGGG C

31

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTGGTGCTA GCTGAGGAGA CG

22

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CATCTAGATG GCGCCGCCAC AGTACGTTTG ATCTCCAGCT TGGTCCC

47

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AAGGCCTCCC AAAGTGTGA TTATGATGGT GATAGTTATA TGAAC

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACCTCCGTA TGGGTGTTTC C

21

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACATCTACT GGGACGACGA CAAACGTTAC AACCCGAGCC TGAAATCC

48

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(11) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGAAACCG TTTTCTACTG GTACTTCGAC GTT

33

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		
GTC	CAC	TCC	GAT	ATC	GTG	ATG	ACC	CAG	TCT	CCA	GAC	TCG	CTA	GCT	GTG	96
Val	His	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	
			20					25					30			
TCT	CTG	GGC	GAG	AGG	GCC	ACC	ATC	AAC	TGC	AAG	GCC	TCC	CAA	AGT	GTT	144
Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ala	Ser	Gln	Ser	Val	
		35					40					45				

GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG	192
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG	240
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly	
65 70 75 80	
GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC	288
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85 90 95	
ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG	336
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln	
100 105 110	
CAA AGT AAT GAG GAT CCT CCG ACG TTC GGC GGA GGG ACC AAA GTG GAG	384
Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu	
115 120 125	
ATC AAA CGT	393
Ile Lys Arg	
130	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
20 25 30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val
35 40 45

Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
100 105 110

Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg
130